AMENDMENTS TO THE SPECIFICATION

Please amend the specification as shown below and insert the 'Sequence Listing' that is being submitted with the accompanying "SUBMISSION OF "SEQUENCE LISTING," COMPUTER READABLE COPY, AND/OR AMENDMENT PERTAINING THERETO FOR BIOTECHNOLOGY INVENTION CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE" after the last paragraph of the specification and before the claims.

(Page 4, paragraph 2, currently amended)

In accordance with the purposes of the present invention, as embodied and broadly described herein, the present invention includes a method for detecting a binding event between at least one binder and members of a receptor array. The method comprises the steps of exposing a plurality of receptors to at least one potential binder; arraying the receptors onto a substrate; exposing each member of the array that has already been exposed to potential binders to X-ray radiation to induce an X-ray fluorescence signal from each member of the array now bound to at least one binder, thereby indicating that a binding event has occurred; and detecting an X-ray ~~fluorescent signal~~ fluorescence signal resulting from exposure to the X-ray radiation from any member of the array where a binding event has occurred.

(Page 5, paragraph 3, currently amended)

The method of the present invention was demonstrated with a polymer bead-supported oligopeptide library purchased from Biopeptide Co., a commercial vendor. The library consisted of 625 unique 11-mer oligopeptides, i.e. each oligopeptide had a unique sequence of 11 amino acids. The oligopeptides used had the following general formula: ~~NH_2-x-Gly-Gly-x-Gly-Gly-x-Gly-Gly-x-Phe-polymer~~ XaaGlyGlyXaaGlyGlyXaaGlyGlyXaaPhe (SEQ ID NO:1). In this formula, ~~"Phe-polymer" indicates that a~~ the phenylalanine (Phe) amino acid of the oligopeptide is chemically bonded to the polymer bead support. The abbreviations for the amino acids in this formula are standard three-letter abbreviations used for the α-amino acids found in proteins and can be found in many textbooks (for example, see table 29.1 in F. A. Carey, Organic Chemistry, McGraw-Hill, 1987, pp. 1086-1087). In the formula: Phe is phenylalanine; Gly is glycine, ~~NH_2 is the amine end group of the last amino acid of the chain,~~ and ~~x~~ Xaa is any one of the following five amino acids: histidine (His); arginine (Arg); serine (Ser); tryptophan (Trp); and tyrosine (Tyr). Permutation of these amino acids among the four '~~x~~ X' positions generates a library of 625 unique 11-mer oligopeptides.

(Page 7, paragraph 3, currently amended)

The method of the invention, in particular, was used to detect binding of N,N-diethylaminoethanethiol and/or methylphosphonic acid with members of the 11-mer oligopeptide library. An aqueous solution of these materials was prepared by combining 0.2 mL of a 200 mM solution of methylphosphonic acid (40 μmol) with 0.2 mL of a 210 mM solution of the hydrogen chloride salt of N,N-diethylaminoethanethiol (42 μmol). About 2500 of the oligopeptide-supported beads (corresponding to 5 mg total weight with about 1.6 μmol total oligopeptide) were incubated in the solution at room temperature for 2 days. The beads were then removed from solution, washed with 10 mL of water, air dried, and immobilized on a tacky dot™ plate as an array. The beads of the array were then analyzed for binding using micro-X-ray fluorescence spectrometry using the EDAX micro-fluorescence instrument. Two beads in particular displayed a strong binding effect with methylphosphonic acid. Their amino acid sequences, as determined by Edman degradation analysis, were the following (the amine end group belongs to the amino acid at the end of the chain): 1) ~~NH_2-His-Gly-Gly-His-Gly-Gly-His-Gly-Gly-Arg-Phe~~ HisGlyGlyHisGlyGlyHisGlyGlyArgPhe (SEQ ID NO:2); and 2) ~~NH_2-Tyr-Gly-Gly-Tyr-Gly-Gly-Trp-Gly-Gly-Tyr-Phe~~ TyrGlyGlyTyrGlyGlyTrpGlyGlyTyrPhe (SEQ ID NO:3). Two different beads displayed a strong binding effect with the thiol. Their amino acid sequences, as determined by Edman degradation analysis, were the following: 3) ~~NH_2-Ser-Gly-Gly-Arg-Gly-Gly-His-Gly-Gly-His-Phe~~ SerGlyGlyArgGlyGlyHisGlyGlyHisPhe (SEQ ID NO:4); and 4) ~~NH_2-Trp-Gly-Gly-His-Gly-Gly-His-Gly-Gly-Trp-Phe~~ TrpGlyGlyHisGlyGlyHisGlyGlyTrpPhe (SEQ ID NO:5).